WHAT IS CLAIMED IS:

1. A substantially pure α-conotoxin peptide having the generic formula I: Xaa$_1$-Xaa$_2$-Xaa$_3$-Xaa$_4$-Xaa$_5$-Cys-Cys-Xaa$_6$-Xaa$_7$-Xaa$_8$-Xaa$_9$-Cys-Xaa$_{10}$-Xaa$_{11}$-Xaa$_{12}$-Cys-Xaa$_{13}$ (SEQ ID NO1:), wherein Xaa$_1$ is des-Xaa$_1$, Ile, Leu or Val; Xaa$_2$ is des-Xaa$_2$, Ala or Gly; Xaa$_3$ is des-Xaa$_3$, Gly, Trp (D or L), neo-Trp, halo-Trp or any unnatural aromatic amino acid; Xaa$_4$ is des-Xaa$_4$, Asp, Phe, Gly, Ala, Glu,γ-carboxy-Glu (Gla) or any unnatural aromatic amino acid; Xaa$_5$ is Glu, Gla, Asp, Ala, Thr, Ser, Gly, Ile, Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr or any unnatural hydroxy containing amino acid; Xaa$_6$ is Ser, Thr, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; Xaa$_7$ is Asp, Glu, Gla, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; Xaa$_8$ is Ser, Thr, Asn, Ala, Gly, His, halo-His, Pro or hydroxy-Pro; Xaa$_9$ is Thr, Ser, Ala, Asp, Asn, Pro, hydroxy-Pro, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; Xaa$_{10}$ is Gly, Ser, Thr, Ala, Asn, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; Xaa$_{11}$ is Gln, Leu, His, halo-His, Trp (D or L), halo-Trp, neo-Trp, Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys, any unnatural basic amino acid or any unnatural aromatic amino acid; Xaa$_{12}$ is Asn, His, halo-His, Ile, Leu, Val, Gln, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; Xaa$_{13}$ is des-Xaa$_{13}$, Val, Ile, Leu, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; and the C-terminus contains a free carboxyl group or an amide group.

2. A substantially pure α-conotoxin peptide of generic formula I selected from the group consisting of:

Asp-Xaa$_1$-Cys-Cys-Ser-Asp-Ser-Arg-Cys-Gly-Xaa$_2$-Asn-Cys-Leu (SEQ ID NO:4);

Ala-Cys-Cys-Ser-Asp-Arg-Arg-Cys-Arg-Xaa$_3$-Arg-Cys (SEQ ID NO:5);

Phe-Thr-Cys-Cys-Arg-Arg-Gly-Thr-Cys-Ser-Gln-His-Cys (SEQ ID NO:6);

Asp-Xaa$_4$-Cys-Cys-Arg-Arg-His-Ala-Cys-Thr-Leu-Ile-Cys (SEQ ID NO:7);

Asp-Xaa$_4$-Cys-Cys-Arg-Xaa$_5$-Xaa$_5$-Cys-Thr-Leu-Ile-Cys (SEQ ID NO:8);

Gly-Cys-Cys-Ser-Asp-Xaa$_5$-Arg-Cys-Arg-Xaa$_4$-Arg-Cys-Arg (SEQ ID NO:9);

Gly-Gly-Cys-Cys-Ser-Asp-Xaa$_5$-Arg-Cys-Ala-Xaa$_3$-Arg-Cys (SEQ ID NO:10);

Ile-Ala-Xaa$_3$-Asp-Ile-Cys-Cys-Ser-Xaa$_1$-Xaa$_5$-Asp-Cys-Asn-His-Xaa$_2$-Cys-Val(SEQ ID NO:11); and

Gly-Cys-Cys-Ser-Asp-Xaa$_5$-Arg-Cys-Xaa$_2$-His-Gln-Cys (SEQ ID NO:12),

wherein Xaa$_1$ is Glu or γ-carboxy-Glu (Gla); Xaa$_2$ is Lys, N-methyl-Lys, N,N-dimethyl-Lys or N,N,N-trimethyl-Lys; Xaa$_3$ is Trp (D or L), halo-Trp or neo-Trp; Xaa$_4$ is Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr or nitro-Tyr; and Xaa$_5$ is Pro or hydroxy-Pro; and the C-terminus contains a carboxyl or amide group, or derivatives thereof.

3.   The substanially pure α-conotoxin peptide of claim 2, wherein Xaa$_1$ is Glu.

4.   The substantially pure α-conotoxin peptide of claim 2, wherein Xaa$_2$ is Lys.

5.   The substantially pure α-conotoxin peptide of claim 2, wherein Xaa$_4$ is Tyr.

6.   The substantially pure α-conotoxin peptide of claim 2, wherein Xaa$_4$ is mono-iodo-Tyr.

7.   The substantially pure α-conotoxin peptide of claim 2, wherein Xaa$_4$ is di-iodo-Tyr.

8.   The substantially pure α-conotoxin peptide of claim 1, which is modified to contain an O-glycan, an S-glycan or an N-glycan.

9   The substantially pure α-conotoxin peptide of claim 2 which is modified to contain an O-glycan, an S-glycan or an N-glycan.

10   A substantially pure α-conotoxin peptide having the generic formula II: Xaa$_1$-Xaa$_2$-Xaa$_3$-Xaa$_4$-Cys-Cys-Xaa$_5$-Xaa$_6$-Xaa$_7$-Xaa$_8$-Cys-Xaa$_9$-Xaa$_{10}$-Xaa$_{11}$-Xaa$_{12}$-Xaa$_{13}$-Xaa$_{14}$-Cys-Xaa$_{15}$-Xaa$_{16}$-Xaa$_{17}$ (SEQ ID NO:2), wherein Xaa$_1$ is des-Xaa$_1$, Asp, Glu or γ-carboxy-Glu (Gla);

Xaa_2 is des-Xaa_2, Gln, Ala, Asp, Glu, Gla; Xaa_3 is des-Xaa_3, Gly, Ala, Asp, Glu, Gla, Pro or hydroxy-Pro; Xaa_4 is des-Xaa_4, Gly, Glu, Gla, Gln, Asp, Asn, Pro or hydroxy-Pro; Xaa_5 is Ser, Thr, Gly, Glu, Gla, Asn, Trp (D or L), neo-Trp, halo-Trp, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys, any unnatural basic amino acid, Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr or any unnatural hydroxy containing amino acid; Xaa_6 is Asp, Asn, His, halo-His, Thr, Ser, Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr or any unnatural hydroxy containing amino acid; Xaa_7 is Pro or hydroxy-Pro; Xaa_8 is Ala, Ser, Thr, Asp, Val, Ile, Pro, hydroxy-Pro, Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr or any unnatural hydroxy containing amino acid; Xaa_9 is Gly, Ile, Leu, Val, Ala, Thr, Ser, Pro, hydroxy-Pro, Phe, Trp (D or L), neo-Trp, halo-Trp, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys, any unnatural basic amino acid or any unnatural aromatic amino acid; Xaa_{10} is Ala, Asn, Phe, Pro, hydroxy-Pro, Glu, Gla, Gln, His, halo-His, Val, Ser, Thr, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; Xaa_{11} is Thr, Ser, His, halo-His, Leu, Ile, Val, Asn, Met, Pro, hydroxy-Pro, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys, any unnatural basic amino acid, Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr or any unnatural hydroxy containing amino acid; Xaa_{12} is Asn, Pro, hydroxy-Pro, Gln, Ser, Thr, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys N,N,N-trimethyl-Lys, any unnatural basic amino acid, Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr or any unnatural hydroxy containing amino acid; Xaa_{13} is des-Xaa_{13}, Gly, Thr, Ser, Pro, hydroxy-Pro, Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr or any unnatural hydroxy containing amino acid; Xaa_{14} is des-Xaa_{14}, Ile, Val, Asp, Leu, Phe, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys, any unnatural basic amino acid, Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr or any unnatural hydroxy containing amino acid; and Xaa_{15} is des-Xaa_{15}, Gly, Ala, Met, Ser, Thr, Trp (D or L), neo-Trp, halo-Trp, any unnatural aromatic amino acid, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; Xaa_{16} is des-Xaa_{16}, Trp (D or L), neo-Trp, halo-Trp, any unnatural aromatic amino acid, Arg, ornithine, homoarginine, Lys, N-methyl-

Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; Xaa_{17} is des-Xaa_{17}, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; and the C-terminus contains a free carboxyl group or an amide group.

11. A substantially pure α-conotoxin peptide of generic formula II seleceted from the group consisting of:

Cys-Cys-Ser-Asp-Xaa_5-Ala-Cys-Xaa_2-Gln-Thr-Xaa_5-Gly-Cys-Arg (SEQ ID NO:13);

Cys-Cys-Xaa_1-Asn-Xaa_5-Ala-Cys-Arg-His-Thr-Gln-Gly-Cys (SEQ ID NO:14);

Gly-Cys-Cys-Xaa_3-His-Xaa_5-Ala-Cys-Gly-Arg-His-Xaa_4-Cys (SEQ ID NO:15);

Ala-Xaa_5-Cys-Cys-Asn-Asn-Xaa_5-Ala-Cys-Val-Xaa_2-His-Arg-Cys (SEQ ID NO:16);

Ala-Xaa_5-Gly-Cys-Cys-Asn-Asn-Xaa_5-Ala-Cys-Val-Xaa_2-His-Arg-Cys (SEQ ID NO:17);

Xaa_5-Xaa_5-Cys-Cys-Asn-Asn-Xaa_5-Ala-Cys-Val-Xaa_2-His-Arg-Cys (SEQ ID NO:18);

Asp-Xaa_1-Asn-Cys-Cys-Xaa_3-Asn-Xaa_5-Ser-Cys-Xaa_5-Arg-Xaa_5-Arg-Cys-Thr (SEQ ID NO:19);

Gly-Cys-Cys-Ser-Thr-Xaa_5-Xaa_5-Cys-Ala-Val-Leu-Xaa_4-Cys (SEQ ID NO:20);

Gly-Cys-Cys-Gly-Asn-Xaa_5-Asp-Cys-Thr-Ser-His-Ser-Cys (SEQ ID NO:21);

Gly-Cys-Cys-Ser-Asn-Xaa_5-Xaa_5-Cys-Ala-His-Asn-Asn-Xaa_5-Asp-Cys-Arg (SEQ ID NO:42);

Gly-Cys-Cys-Xaa_4-Asn-Xaa_5-Val-Cys-Xaa_2-Xaa_2-Xaa_4-Xaa_4-Cys-Xaa_3-Xaa_2 (SEQ ID NO:154);

Xaa_6-Xaa_1-Xaa_5-Gly-Cys-Cys-Arg-His-Xaa_5-Ala-Cys-Gly-Xaa_2-Asn-Arg-Cys (SEQ ID NO:155);

Cys-Cys-Ala-Asp-Xaa_5-Asp-Cys-Arg-Phe-Arg-Xaa_5-Gly-Cys (SEQ ID NO:156);

Gly-Cys-Cys-Xaa_4-Asn-Xaa_5-Ser-Cys-Xaa_3-Xaa_5-Xaa_2-Thr-Xaa_4-Cys-Ser-Xaa_3-Xaa_2 (SEQ ID NO:157);

Cys-Cys-Ser-Asn-Xaa_5-Thr-Cys-Xaa_2-Xaa_1-Thr-Xaa_4-Gly-Cys (SEQ ID NO:158);

Cys-Cys-Ala-Asn-Xaa_5-Ile-Cys-Xaa_2-Asn-Thr-Xaa_5-Gly-Cys (SEQ ID NO:159);

Cys-Cys-Asn-Asn-Xaa_5-Thr-Cys-Xaa_2-Xaa_1-Thr-Xaa_4-Gly-Cys (SEQ ID NO:160);

Cys-Cys-Ser-Asn-Xaa_5-Val-Cys-Xaa_2-Xaa_1-Thr-Xaa_4-Gly-Cys (SEQ ID NO:161);

Gly-Gly-Cys-Cys-Ser-Xaa₄-Xaa₅-Xaa₅-Cys-Ile-Ala-Ser-Asn-Xaa₅-Xaa₂-Cys-Gly (SEQ ID NO:162);

Gly-Cys-Cys-Ser-His-Xaa₅-Val-Cys-Ser-Ala-Met-Ser-Xaa₅-Ile-Cys (SEQ ID NO:163);

Gly-Cys-Cys-Xaa₂-Asn-Xaa₅-Xaa₄-Cys-Gly-Ala-Ser-Xaa₂-Thr-Xaa₄-Cys (SEQ ID NO:164);

Gly-Cys-Cys-Ser-Xaa₄-Xaa₅-Xaa₅-Cys-Phe-Ala-Thr-Asn-Xaa₅-Asp-Cys (SEQ ID NO:165);

Gly-Gly-Cys-Cys-Ser-Xaa₄-Xaa₅-Xaa₅-Cys-Ile-Ala-Asn-Asn-Xaa₅-Leu-Cys-Ala (SEQ ID NO:166);

Gly-Gly-Cys-Cys-Ser-Xaa₄-Xaa₅-Xaa₅-Cys-Ile-Ala-Asn-Asn-Xaa₅-Phe-Cys-Ala (SEQ ID NO:167);

Asp-Cys-Cys-Ser-Asn-Xaa₅-Xaa₅-Cys-Ser-Gln-Asn-Asn-Xaa₅-Asp-Cys-Met (SEQ ID NO:168); and

Asp-Cys-Cys-Ser-Asn-Xaa₅-Xaa₅-Cys-Ala-His-Asn-Asn-Xaa₅-Asp-Cys-Arg (SEQ ID NO:169),

wherein Xaa_1 is Glu or γ-carboxy-Glu (Gla); Xaa_2 is Lys, N-methyl-Lys, N,N-dimethyl-Lys or N,N,N-trimethyl-Lys; Xaa_3 is Trp (D or L), halo-Trp or neo-Trp; Xaa_4 is Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr or nitro-Tyr; and Xaa_5 is Pro or hydroxy-Pro; and the C-terminus contains a carboxyl or amide group, or derivatives thereof.

12. The substantially pure α-conotoxin peptide of claim 11, wherein Xaa_2 is Lys.

13. The substantially pure α-conotoxin peptide of claim 11, wherein Xaa_1 is Glu.

14. The substantially pure α-conotoxin peptide of claim 11, wherein Xaa_3 is Trp.

15. The substantially pure α-conotoxin peptide of claim 11, wherein Xaa_4 is Tyr.

16. The substantially pure α-conotoxin peptide of claim 11, wherein Xaa_4 is mono-iodo-Tyr.

17. The substantially pure α-conotoxin peptide of claim 11, wherein Xaa_4 is di-iodo-Tyr.

18. The substantially pure α-conotoxin peptide of claim 10, which is modified to contain an O-glycan, an S-glycan or an N-glycan.

19 The substantially pure α-conotoxin peptide of claim 11 which is modified to contain an O-glycan, an S-glycan or an N-glycan.

20. A substantially pure α-conotoxin peptide having the generic formula III: Xaa_1-Xaa_2-Xaa_3-Xaa_4-Xaa_5-Cys-Cys-Xaa_6-Xaa_7-Xaa_8-Xaa_9-Cys-Xaa_{10}-Xaa_{11}-Xaa_{12}-Xaa_{13}-Xaa_{14}-Xaa_{15}-Xaa_{16}-Cys-Xaa_{17}-Xaa_{18}-Xaa_{19}-Xaa_{20}-Xaa_{21}-Xaa_{22}-Xaa_{23}-Xaa_{24} (SEQ ID NO:3), wherein Xaa_1 is des-Xaa_1, Ser or Thr; Xaa_2 is des-Xaa_2, Asp, Glu, γ-carboxy-Glu (Gla), Asn, Ser or Thr; Xaa_3 is des-Xaa_3, Ala, Gly, Asn, Ser, Thr, Pro, hydroxy-Pro, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; Xaa_4 is des-Xaa_4, Ala, Val, Leu, Ile, Gly, Glu, Gla, Gln, Asp, Asn, Phe, Pro, hydroxy-Pro or any unnatural aromatic amino acid; Xaa_5 is des-Xaa_5, Thr, Ser, Asp, Glu, Gla, Gln, Gly, Val, Asp, Asn, Ala, Pro, hydroxy-Pro, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; Xaa_6 is Thr, Ser, Asp, Asn, Met, Val, Ala, Gly, Leu, Ile, Phe, any unnatural aromatic amino acid, Pro, hydroxy-Pro, Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr or any unnatural hydroxy containing amino acid; Xaa_7 is Ile, Leu, Val, Ser, Thr, Gln, Asn, Asp, Arg, His, halo-His, Phe, any unnatural aromatic amino acid, homoarginine, ornithine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys, any unnatural basic amino acid, Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr or any unnatural hydroxy containing amino acid; Xaa_8 is Pro, hyroxy-Pro, Ser, Thr, Ile, Asp, Leu, Val, Gly, Ala, Phe, any unnatural aromatic amino acid, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; Xaa_9 is Val, Ala, Gly, Ile, Leu, Asp, Ser, Thr, Pro, hydroxy-Pro, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; Xaa_{10} is His, halo-His, Arg, homoarginine, ornithine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys, any unnatural basic amino acid, Asn, Ala, Ser, Thr, Phe, Ile, Leu, Gly, Trp (D or L), neo-Trp, halo-Trp, any unnatural aromatic amino acid, Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr or any unnatural hydroxy containing amino acid; Xaa_{11} is Leu, Gln, Val, Ile,

Gly, Met, Ala, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys, Ser, Thr, Arg, homoarginine, ornithine, any unnatural basic amino acid, Asn, Glu, Gla, Gln, Phe, Trp (D or L), neo-Trp, halo-Trp or any unnatural aromatic amino acid; Xaa_{12} is Glu, Gla, Gln, Asn, Asp, Pro, hydroxy-Pro, Ser, Gly, Thr, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys, Arg, homoarginine, ornithine, any unnatural basic amino acid, Phe, His, halo-His, any unnatural aromatic amino acid, Leu, Met, Gly, Ala, Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr or any unnatural hydroxy containing amino acid; Xaa_{13} is His, halo-His, Asn, Thr, Ser, Ile, Val, Leu, Phe, any unnatural aromatic amino acid, Arg, homoarginine, ornithine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys, any unnatural basic amino acid, Tyr, nor-Try, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr or any unnatural hydroxy containing amino acid; Xaa_{14} is Ser, Thr, Ala, Gln, Pro, hydroxy-Pro, Gly, Ile, Leu, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; Xaa_{15} is Asn, Glu, Gla, Asp, Gly, His, halo-His, Ala, Leu, Gln, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys, any unnatural basic amino acid, Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr or any unnatural hydroxy containing amino acid; Xaa_{16} is Met, Ile, Thr, Ser, Val, Leu, Pro, hydroxy-Pro, Phe, any unnatural aromatic amino acid, Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr, any unnatural hydroxy containing amino acid, Glu, Gla, Ala, His, halo-His, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; Xaa_{17} is des-Xaa_{17}, Gly, Asp, Asn, Ala, Ile, Leu, Ser, Thr, His, halo-His, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; Xaa_{18} is des-Xaa_{18}, Gly, Glu, Gla, Gln, Trp (D or L), neo, halo-Trp, any unnatural aromatic amino acid, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; Xaa_{19} is des-Xaa_{19}, Ser, Thr, Val, Ile, Ala, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; Xaa_{20} is des-Xaa_{20}, Val, Asp, His, halo-His, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; Xaa_{21} is des-Xaa_{21}, Asn, Pro or hydroxy-Pro; Xaa_{22} is des-Xaa_{22}, Arg, ornithine, homoarginine, Lys, N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any unnatural basic amino acid; Xaa_{23} is des-Xaa_{23},

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Ser or Thr; Xaa$_{24}$ is des-Xaa$_{24}$, Leu, Ile or Val; and the C-terminus contains a free carboxyl group or an amide group, with the proviso that (a) Xaa$_5$ is not Gly, when Xaa$_1$ is des-Xaa$_1$, Xaa$_2$ is des-Xaa$_2$, Xaa$_3$ is des-Xaa$_3$, Xaa$_4$ is des-Xaa$_4$, Xaa$_6$ is Ser, Xaa$_7$ is His, Xaa$_8$ is Pro, Xaa$_9$ is Ala, Xaa$_{10}$ is Ser, Xaa$_{11}$ is Val, Xaa$_{12}$ is Asn, Xaa$_{13}$ is Asn, Xaa$_{14}$ is Pro, Xaa$_{15}$ is Asp, Xaa$_{16}$ is Ile, Xaa$_{17}$ is des-Xaa$_{17}$, Xaa$_{18}$ is des-Xaa$_{18}$, Xaa$_{19}$ is des-Xaa$_{19}$, Xaa$_{20}$ is des-Xaa$_{20}$, Xaa$_{21}$ is des-Xaa$_{21}$, Xaa$_{22}$ is des-Xaa$_{22}$, Xaa$_{23}$ is des-Xaa$_{23}$, and Xaa$_{24}$ is des-Xaa$_{24}$.

21. A substantially pure α-conotoxin peptide of generic formula III selected from the group consisting of:

Gly-Cys-Cys-Ser-Asn-Xaa$_5$-Val-Cys-His-Leu-Xaa$_1$-His-Ser-Asn-Met-Cys (SEQ ID NO:22);

Gly-Cys-Cys-Ser-Asn-Xaa$_5$-Val-Cys-Arg-Gln-Asn-Asn-Ala-Xaa$_1$-Xaa$_4$-Cys-Arg (SEQ ID NO:23);

Xaa$_5$-Gln-Cys-Cys-Ser-His-Xaa$_5$-Ala-Cys-Asn-Val-Asp-His-Xaa$_5$-Xaa$_1$-Ile-Cys-Arg (SEQ ID NO:24);

Xaa$_5$-Xaa$_1$-Cys-Cys-Ser-His-Xaa$_5$-Ala-Cys-Asn-Val-Asp-His-Xaa$_5$-Xaa$_1$-Ile-Cys-Arg (SEQ ID NO:25);

Xaa$_5$-Gln-Cys-Cys-Ser-His-Xaa$_5$-Ala-Cys-Asn-Val-Asp-His-Xaa$_5$-Xaa$_1$-Ile-Cys-Asp (SEQ ID NO:26);

Xaa$_5$-Arg-Cys-Cys-Ser-His-Xaa$_5$-Ala-Cys-Asn-Val-Asp-His-Xaa$_5$-Xaa$_1$-Ile-Cys-Arg (SEQ ID NO:27);

Xaa$_5$-Gln-Cys-Cys-Ser-His-Xaa$_5$-Ala-Cys-Asn-Val-Asp-His-Xaa$_5$-Gly-Ile-Cys-Arg (SEQ ID NO:28);

Xaa$_5$-Gln-Cys-Cys-Ser-His-Xaa$_5$-Ala-Cys-Asn-Val-Asp-His-Xaa$_5$-Xaa$_1$-Thr-Cys-Arg (SEQ ID NO:29);

Xaa$_5$-Gln-Cys-Cys-Ser-His-Xaa$_5$-Ala-Cys-Asn-Val-Asp-His-Xaa$_5$-Xaa$_1$-Val-Cys-Arg (SEQ ID NO:30);

Xaa$_5$-Gln-Cys-Cys-Ser-His-Xaa$_5$-Ala-Cys-Asn-Ile-Asp-His-Xaa$_5$-Xaa$_1$-Ile-Cys-Arg (SEQ ID NO:31);

Xaa$_5$-Gln-Cys-Cys-Ser-His-Xaa$_5$-Ala-Cys-Asn-Val-Asp-His-Xaa$_5$-Xaa$_1$-Ile-Cys-Arg-Arg-Arg-Arg (SEQ ID NO:32);

Gly-Gly-Cys-Cys-Ser-His-Xaa$_5$-Ala-Cys-Ala-Val-Asn-His-Xaa$_5$-Xaa$_1$-Leu-Cys (SEQ ID NO:33);

Gly-Cys-Cys-Ser-His-Xaa$_5$-Ala-Cys-Ser-Val-Asn-His-Xaa$_5$-Xaa$_1$-Leu-Cys (SEQ ID NO:34);

Gly-Cys-Cys-Ser-His-Xaa$_5$-Ala-Cys-Asn-Val-Asp-His-Xaa$_5$-Xaa$_1$-Ile-Cys (SEQ ID NO:35);

Gly-Cys-Cys-Ser-His-Xaa$_5$-Ala-Cys-Ser-Gly-Xaa$_1$-Thr-Gln-Xaa$_1$-Xaa$_5$-Cys-Arg-Xaa$_1$-Ser (SEQ ID NO:36);

Xaa$_5$-Cys-Cys-Ser-His-Xaa$_5$-Ala-Cys-Ser-Gly-Asn-Asn-Xaa$_5$-Xaa$_1$-Phe-Cys-Arg-Gln (SEQ ID NO:37);

Gly-Cys-Cys-Ser-His-Xaa$_5$-Ala-Cys-Ser-Gly-Asn-Asn-Xaa$_5$-Xaa$_1$-Phe-Cys-Arg-Gln (SEQ ID NO:38);

Gly-Cys-Cys-Ser-His-Xaa$_5$-Xaa$_5$-Cys-Ala-Met-Asn-Asn-Xaa$_5$-Asp-Xaa$_4$-Cys (SEQ ID NO:39);

Gly-Cys-Cys-Ser-His-Xaa$_5$-Xaa$_5$-Cys-Phe-Leu-Asn-Asn-Xaa$_5$-Asp-Xaa$_4$-Cys (SEQ ID NO:40);

Gly-Cys-Cys-Ser-Asn-Xaa$_5$-Xaa$_5$-Cys-Ile-Ala-Xaa$_2$-Asn-Xaa$_5$-His-Met-Cys-Gly (SEQ ID NO:41);

Gly-Cys-Cys-Ser-Asn-Xaa$_5$-Ala-Cys-Ala-Gly-Asn-Asn-Xaa$_5$-His-Val-Cys-Arg-Gln (SEQ ID NO:43);

Gly-Cys-Cys-Ser-Arg-Xaa$_5$-Ala-Cys-Ile-Ala-Asn-Asn-Xaa$_5$-Asp-Leu-Cys (SEQ ID NO:44);

Gly-Cys-Cys-Ser-Asn-Xaa$_5$-Val-Cys-His-Val-Xaa$_1$-His-Xaa$_5$-Xaa$_1$-Leu-Cys-Arg-Arg-Arg-Arg (SEQ ID NO:45);

Gly-Gly-Cys-Cys-Ser-Phe-Xaa$_5$-Ala-Cys-Arg-Xaa$_2$-Xaa$_5$-Arg-Xaa$_5$-Xaa$_1$-Met-Cys-Gly (SEQ ID NO:46);

Xaa$_5$-Xaa$_1$-Cys-Cys-Ser-Asp-Xaa$_5$-Arg-Cys-Asn-Ser-Ser-His-Xaa$_5$-Xaa$_1$-Leu-Cys-Gly (SEQ ID NO:47);

Xaa$_5$-Gln-Cys-Cys-Ser-Asp-Xaa$_5$-Arg-Cys-Asn-Val-Gly-His-Xaa$_5$-Xaa$_1$-Leu-Cys-Gly (SEQ ID NO:48);

Xaa$_6$-Val-Cys-Cys-Ser-Asp-Xaa$_5$-Arg-Cys-Asn-Val-Gly-His-Xaa$_5$-Xaa$_1$-Ile-Cys-Gly (SEQ ID NO:49);

Gly-Cys-Cys-Ser-Arg-Xaa$_5$-Xaa$_5$-Cys-Ile-Ala-Asn-Asn-Xaa$_5$-Asp-Leu-Cys (SEQ ID NO:50);

Xaa$_5$-Gln-Cys-Cys-Ser-His-Leu-Ala-Cys-Asn-Val-Asp-His-Xaa$_5$-Xaa$_1$-Ile-Cys-Arg (SEQ ID NO:51);

Gly-Cys-Cys-Ser-Xaa$_4$-Phe-Asp-Cys-Arg-Met-Met-Phe-Xaa$_5$-Xaa$_1$-Met-Cys-Gly-Xaa$_3$-Arg (SEQ ID NO:52);

Gly-Gly-Cys-Cys-Ser-Phe-Ala-Ala-Cys-Arg-Xaa$_2$-Xaa$_4$-Arg-Xaa$_5$-Xaa$_1$-Met-Cys-Gly (SEQ ID NO:53);

Gly-Gly-Cys-Cys-Phe-His-Xaa$_5$-Val-Cys-Xaa$_4$-Ile-Asn-Leu-Leu-Xaa$_1$-Met-Cys-Arg-Gln-Arg (SEQ ID NO:54);

Ser-Ala-Thr-Cys-Cys-Asn-Xaa$_4$-Xaa$_5$-Xaa$_5$-Cys-Xaa$_4$-Xaa$_1$-Thr-Xaa$_4$-Xaa$_5$-Xaa$_1$-Ser-Cys-Leu (SEQ ID NO:55);

Ala-Cys-Cys-Ala-Xaa$_4$-Xaa$_5$-Xaa$_5$-Cys-Phe-Xaa$_1$-Ala-Xaa$_4$-Xaa$_5$-Xaa$_1$-Arg-Cys-Leu (SEQ ID NO:56);

Asn-Ala-Xaa$_1$-Cys-Cys-Xaa$_4$-Xaa$_4$-Xaa$_5$-Xaa$_5$-Cys-Xaa$_4$-Xaa$_1$-Ala-Xaa$_4$-Xaa$_5$-Xaa$_1$-Ile-Cys-Leu (SEQ ID NO:57);

Xaa$_1$-Cys-Cys-Thr-Asn-Xaa$_1$-Val-Cys-His-Ala-Xaa$_1$-His-Gln-Xaa$_1$-Leu-Cys-Ala-Arg-Arg-Arg (SEQ ID NO:170);

Gly-Cys-Cys-Ser-Asn-Xaa$_5$-Val-Cys-His-Leu-Xaa$_1$-His-Ser-Asn-Leu-Cys (SEQ ID NO:171);

Xaa$_1$-Cys-Cys-Thr-Asn-Xaa$_5$-Val-Cys-His-Val-Xaa$_1$-His-Gln-Xaa$_1$-Leu-Cys-Ala-Arg-Arg-Arg (SEQ ID NO:172);

Xaa$_6$-Xaa$_1$-Cys-Cys-Ser-Xaa$_4$-Xaa$_5$-Ala-Cys-Asn-Leu-Asp-His-Xaa$_5$-Xaa$_1$-Leu-Cys (SEQ ID NO:173);

Xaa$_5$-Xaa$_1$-Cys-Cys-Ser-Asp-Xaa$_5$-Arg-Cys-Asn-Ser-Thr-His-Xaa$_5$-Xaa$_1$-Leu-Cys-Gly (SEQ ID NO:174);

Leu-Asn-Cys-Cys-Met-Ile-Xaa$_5$-Xaa$_5$-Cys-Xaa$_3$-Xaa$_2$-Xaa$_2$-Xaa$_4$-Gly-Asp-Arg-Cys-Ser-Xaa$_1$-Val-Arg (SEQ ID NO:175);

Ala-Phe-Gly-Cys-Cys-Asp-Leu-Ile-Xaa$_5$-Cys-Leu-Xaa$_1$-Arg-Xaa$_4$-Gly-Asn-Arg-Cys-Asn-Xaa$_1$-Val-His (SEQ ID NO:176);

Leu-Gly-Cys-Cys-Asn-Val-Thr-Xaa$_5$-Cys-Xaa$_3$-Xaa$_1$-Xaa$_2$-Xaa$_4$-Gly-Asp-Xaa$_2$-Cys-Asn-Xaa$_1$-Val-Arg (SEQ ID NO:177);

Asp-Xaa$_1$-Cys-Cys-Ser-Asn-Xaa$_5$-Ala-Cys-Arg-Val-Asn-Asn-Xaa$_5$-His-Val-Cys-Arg-Arg-Arg (SEQ ID NO:178);

Leu-Asn-Cys-Cys-Ser-Ile-Xaa$_5$-Gly-Cys-Xaa$_3$-Asn-Xaa$_1$-Xaa$_4$-Xaa$_2$-Asp-Arg-Cys-Ser-Xaa$_2$-Val-Arg (SEQ ID NO:179);

Gly-Gly-Cys-Cys-Ser-His-Xaa$_5$-Val-Cys-Xaa$_4$-Phe-Asn-Asn-Xaa$_5$-Gln-Met-Cys-Arg (SEQ ID NO:180);

Gly-Gly-Cys-Cys-Ser-His-Xaa$_5$-Val-Cys-Asn-Leu-Asn-Asn-Xaa$_5$-Gln-Met-Cys-Arg (SEQ ID NO:181);

Gly-Cys-Cys-Ser-His-Xaa$_5$-Xaa$_5$-Cys-Xaa$_4$-Ala-Asn-Asn-Gln-Ala-Xaa$_4$-Cys-Asn (SEQ ID NO:182);

Gly-Gly-Cys-Cys-Ser-His-Xaa$_5$-Ala-Cys-Ser-Val-Thr-His-Xaa$_5$-Xaa$_1$-Leu-Cys(SEQ ID NO:183);

Gly-Gly-Cys-Cys-Ser-Xaa$_4$-Xaa$_5$-Ala-Cys-Ser-Val-Xaa$_4$-His-Gln-Asp-Leu-Cys-Asp (SEQ ID NO:184);

Val-Ser-Cys-Cys-Val-Val-Arg-Xaa$_5$-Cys-Xaa$_3$-Ile-Arg-Xaa$_4$-Gln-Xaa$_1$-Xaa$_1$-Cys-Leu-Xaa$_1$-Ala-Asp-Xaa$_5$-Arg-Thr-Leu (SEQ ID NO:185);

Xaa$_6$-Asn-Cys-Cys-Ser-Ile-Xaa$_5$-Gly-Cys-Xaa$_3$-Xaa$_1$-Xaa$_2$-Xaa$_4$-Gly-Asp-Xaa$_2$-Cys-Ser-Xaa$_1$-Val-Arg (SEQ ID NO:186);

Gly-Cys-Cys-Ser-Asn-Xaa$_5$-Val-Cys-His-Leu-Xaa$_1$-His-Xaa$_5$-Asn-Ala-Cys (SEQ ID NO:187);

Gly-Cys-Cys-Ser-Asn-Xaa$_5$-Ile-Cys-Xaa$_4$-Phe-Asn-Asn-Xaa$_5$-Arg-Ile-Cys-Arg(SEQ ID NO:188);

Xaa$_1$-Cys-Cys-Ser-Gln-Xaa$_5$-Xaa$_5$-Cys-Arg-Xaa$_3$-Xaa$_2$-His-Xaa$_5$-Xaa$_1$-Leu-Cys-Ser (SEQ ID NO:189);

Gly-Cys-Cys-Ser-His-Xaa$_5$-Ala-Cys-Ala-Gly-Asn-Asn-Gln-His-Ile-Cys (SEQ ID NO:190);

Gly-Cys-Cys-Ala-Val-Xaa$_5$-Ser-Cys-Arg-Leu-Arg-Asn-Xaa$_5$-Asp-Leu-Cys-Gly-Gly (SEQ ID NO:191);

Gly-Cys-Cys-Ser-His-Xaa$_5$-Ala-Cys-Asn-Val-Asn-Asn-Xaa$_5$-His-Ile-Cys (SEQ ID NO:192);

Thr-Xaa$_5$-Xaa$_1$-Xaa$_1$-Cys-Cys-Xaa$_5$-Asn-Xaa$_5$-Xaa$_5$-Cys-Phe-Ala-Thr-Asn-Ser-Asp-Ile-Cys-Gly (SEQ ID NO:193);

Asp-Ala-Cys-Cys-Ser-Asp-Xaa$_5$-Arg-Cys-Ser-Gly-Xaa$_2$-His-Gln-Asp-Leu-Cys(SEQ ID NO:194);

Xaa$_1$-Asp-Cys-Cys-Ser-Asp-Xaa$_5$-Arg-Cys-Ser-Val-Gly-His-Gln-Asp-Leu-Cys(SEQ ID NO:195);

Gly-Cys-Cys-Ser-His-Xaa$_5$-Ala-Cys-Ala-Gly-Ser-Asn-Ala-His-Ile-Cys (SEQ ID NO:196);

Xaa$_1$-Asp-Cys-Cys-Ser-Asp-Xaa$_5$-Arg-Cys-Ser-Val-Gly-His-Gln-Asp-Met-Cys (SEQ ID NO:197);

Gly-Cys-Cys-Ser-His-Xaa$_5$-Ala-Cys-Ala-Gly-Asn-Asn-Xaa$_5$-His-Ile-Cys (SEQ ID NO:198);

Gly-Cys-Cys-Gly-Asn-Xaa$_5$-Ser-Cys-Ser-Ile-His-Ile-Xaa$_5$-Xaa$_4$-Val-Cys-Asn (SEQ ID NO:199);

Thr-Asp-Ser-Xaa$_1$-Xaa$_1$-Cys-Cys-Leu-Asp-Ser-Arg-Cys-Ala-Gly-Gln-His-Gln-Asp-Leu-Cys-Gly (SEQ ID NO:200);

Gly-Cys-Cys-Ser-Asn-Xaa$_5$-Xaa$_5$-Cys-Xaa$_4$-Ala-Asn-Asn-Gln-Ala-Xaa$_4$-Cys-Asn (SEQ ID NO:201);

Gly-Cys-Cys-Ser-His-Xaa$_5$-Ala-Cys-Ser-Val-Asn-Asn-Xaa$_5$-Asp-Ile-Cys (SEQ ID NO:202);

Gly-Xaa$_2$-Cys-Cys-Ile-Asn-Asp-Ala-Cys-Arg-Ser-Xaa$_2$-His-Xaa$_5$-Gln-Xaa$_4$-Cys-Ser (SEQ ID NO:203);

Gly-Cys-Cys-Xaa$_4$-Asn-Ile-Ala-Cys-Arg-Ile-Asn-Asn-Xaa$_5$-Arg-Xaa$_4$-Cys-Arg(SEQ ID NO:204);

Gly-Cys-Cys-Ser-His-Xaa$_5$-Val-Cys-Arg-Phe-Asn-Xaa$_4$-Xaa$_5$-Xaa$_2$-Xaa$_4$-Cys-Gly (SEQ ID NO:205);

Asp-Xaa$_1$-Cys-Cys-Ala-Ser-Xaa$_5$-Xaa$_5$-Cys-Arg-Leu-Asn-Asn-Xaa$_5$-Xaa$_4$-Val-Cys-His (SEQ ID NO:206);

Gly-Cys-Cys-Ser-Asn-Xaa$_5$-Val-Cys-Xaa$_3$-Gln-Asn-Asn-Ala-Xaa$_1$-Xaa$_4$-Cys-Arg-Xaa$_1$-Ser (SEQ ID NO:207);

Gly-Cys-Cys-Ser-His-Xaa$_5$-Xaa$_5$-Cys-Ala-Gln-Asn-Asn-Gln-Asp-Xaa$_4$-Cys (SEQ ID NO:208);

Gly-Cys-Cys-Ser-His-Xaa$_5$-Ala-Cys-Ser-Gly-Asn-Asn-Arg-Xaa$_1$-Xaa$_4$-Cys-Arg-Xaa$_1$-Ser (SEQ ID NO:209);

Asp-Xaa$_5$-Cys-Cys-Ser-Xaa$_4$-Xaa$_5$-Asp-Cys-Gly-Ala-Asn-His-Xaa$_5$-Xaa$_1$-Ile-Cys-Gly (SEQ ID NO:210);

Xaa$_1$-Cys-Cys-Ser-Gln-Xaa$_5$-Xaa$_5$-Cys-Arg-Xaa$_3$-Xaa$_2$-His-Xaa$_5$-Xaa$_1$-Leu-Cys-Ser (SEQ ID NO:211);

Gly-Cys-Cys-Ser-His-Xaa$_5$-Ala-Cys-Ala-Gly-Asn-Asn-Xaa$_5$-His-Ile-Cys (SEQ ID NO:212);

Gly-Cys-Cys-Ser-Asp-Xaa$_5$-Ser-Cys-Asn-Val-Asn-Asn-Xaa$_5$-Asp-Xaa$_4$-Cys (SEQ ID NO:213);

Xaa$_1$-Xaa$_1$-Cys-Cys-Ser-Asp-Xaa$_5$-Arg-Cys-Ser-Val-Gly-His-Gln-Asp-Met-Cys-Arg (SEQ ID NO:214);

Gly-Gly-Cys-Cys-Ser-Asn-Xaa$_5$-Ala-Cys-Leu-Val-Asn-His-Leu-Xaa$_1$-Met-Cys (SEQ ID NO:215);

Arg-Asp-Xaa$_5$-Cys-Cys-Phe-Asn-Xaa$_5$-Ala-Cys-Asn-Val-Asn-Asn-Xaa$_5$-Gln-Ile-Cys (SEQ ID NO:216);

Cys-Cys-Ser-Asp-Xaa$_5$-Ser-Cys-Xaa$_3$-Arg-Leu-His-Ser-Leu-Ala-Cys-Thr-Gly-Ile-Val-Asn-Arg (SEQ ID NO:217);

Cys-Cys-Thr-Asn-Xaa$_5$-Ala-Cys-Leu-Val-Asn-Asn-Ile-Arg-Phe-Cys-Gly (SEQ ID NO:218);

Asp-Xaa$_1$-Cys-Cys-Ser-Asp-Xaa$_5$-Arg-Cys-His-Gly-Asn-Asn-Arg-Asp-His-Cys-Ala (SEQ ID NO:219);

Asp-Cys-Cys-Ser-His-Xaa$_5$-Leu-Cys-Arg-Leu-Phe-Val-Xaa$_5$-Gly-Leu-Cys-Ile(SEQ ID NO:220);

Gly-Cys-Cys-Ser-His-Xaa$_5$-Val-Cys-Xaa$_2$-Val-Arg-Xaa$_4$-Xaa$_5$-Asp-Leu-Cys-Arg (SEQ ID NO:221);

Gly-Cys-Cys-Ser-His-Xaa$_5$-Ala-Cys-Asn-Val-Asn-Asn-Xaa$_5$-His-Ile-Cys (SEQ ID NO:222);

Gly-Cys-Cys-Ser-His-Xaa$_5$-Val-Cys-Xaa$_2$-Val-Arg-Xaa$_4$-Ser-Asp-Met-Cys(SEQ ID NO:223);

Gly-Gly-Cys-Cys-Ser-His-Xaa$_5$-Ala-Cys-Xaa$_2$-Val-His-Phe-Xaa$_5$-His-Ser-Cys(SEQ ID NO:224);

Val-Cys-Cys-Ser-Asn-Xaa$_5$-Val-Cys-His-Val-Asp-His-Xaa$_5$-Xaa$_1$-Leu-Cys-Arg-Arg-Arg-Arg (SEQ ID NO:225);

Gly-Cys-Cys-Ser-His-Xaa$_5$-Val-Cys-Asn-Leu-Ser-Asn-Xaa$_5$-Gln-Ile-Cys-Arg (SEQ ID NO:226);

Xaa$_6$-Xaa$_1$-Cys-Cys-Ser-His-Xaa$_5$-Ala-Cys-Asn-Val-Asp-His-Xaa$_5$-Xaa$_1$-Ile-Cys-Arg (SEQ ID NO:227);

Gly-Cys-Cys-Ser-Asn-Xaa$_5$-Ala-Cys-Leu-Val-Asn-His-Ile-Arg-Phe-Cys-Gly (SEQ ID NO:228);

Asp-Cys-Cys-Asp-Asp-Xaa$_5$-Ala-Cys-Thr-Val-Asn-Asn-Xaa$_5$-Gly-Leu-Cys-Thr (SEQ ID NO:229); and

Gly-Cys-Cys-Ser-Asn-Xaa$_5$-Xaa$_5$-Cys-Ile-Ala-Xaa$_2$-Asn-Xaa$_5$-His-Met-Cys-Gly-Gly-Arg-Arg (SEQ ID NO:230),

wherein Xaa$_1$ is Glu or γ-carboxy-Glu (Gla); Xaa$_2$ is Lys, N-methyl-Lys, N,N-dimethyl-Lys or N,N,N-trimethyl-Lys; Xaa$_3$ is Trp (D or L), halo-Trp or neo-Trp; Xaa$_4$ is Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr or nitro-Tyr; and Xaa$_5$ is Pro or hydroxy-Pro; Xaa$_6$ is Gln or pyro-Glu; and the C-terminus contains a carboxyl or amide group, or derivatives thereof.

22.   The substantially pure α-conotoxin peptide of claim 21, wherein Xaa$_2$ is Lys.

23.   The substantially pure α-conotoxin peptide of claim 21, wherein Xaa$_1$ is Glu.

24.   The substantially pure α-conotoxin peptide of claim 21, wherein Xaa$_3$ is Trp.

25.   The substantially pure α-conotoxin peptide of claim 21, wherein Xaa$_4$ is Tyr.

26.   The substantially pure α-conotoxin peptide of claim 21, wherein Xaa$_4$ is mono-iodo-Tyr.

27.   The substantially pure α-conotoxin peptide of claim 21, wherein Xaa$_4$ is di-iodo-Tyr.

28.   The substantially pure α-conotoxin peptide of claim 20, which is modified to contain an O-glycan, an S-glycan or an N-glycan.

29   The substantially pure α-conotoxin peptide of claim 21 which is modified to contain an O-glycan, an S-glycan or an N-glycan.

30.   A substantially pure α-conotoxin peptide seleceted from the group consisting of:

Cys-Cys-Thr-Ile-Xaa₅-Ser-Cys-Xaa₄-Xaa₁-Xaa₂-Xaa₂-Xaa₂-Ile-Xaa₂-Ala-Cys-Val-Phe (SEQ ID NO:231) and

Gly-Cys-Cys-Gly-Asn-Xaa₅-Ala-Cys-Ser-Gly-Ser-Ser-Xaa₂-Asp-Ala-Xaa₅-Ser-Cys (SEQ ID NO:232),

wherein Xaa₁ is Glu or γ-carboxy-Glu (Gla); Xaa₂ is Lys, N-methyl-Lys, N,N-dimethyl-Lys or N,N,N-trimethyl-Lys; Xaa₄ is Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr or nitro-Tyr; and Xaa₅ is Pro or hydroxy-Pro; and the C-terminus contains a carboxyl or amide group, or derivatives thereof.

31.   The substantially pure α-conotoxin peptide of claim 30, wherein Xaa₂ is Lys.

32.   The substantially pure α-conotoxin peptide of claim 30, wherein Xaa₁ is Glu.

33.   The substantially pure α-conotoxin peptide of claim 30, wherein Xaa₄ is Tyr.

34.   The substantially pure α-conotoxin peptide of claim 30, wherein Xaa₄ is mono-iodo-Tyr.

35.   The substantially pure α-conotoxin peptide of claim 30, wherein Xaa₄ is di-iodo-Tyr.

36.   The substantially pure α-conotoxin peptide of claim 30, which is modified to contain an O-glycan, an S-glycan or an N-glycan.

37.   An isolated nucleic acid comprising a nucleic acid coding for an α-conotoxin precursor comprising an amino acid sequence selected from the group of amino acid sequences set forth in Tables 1-134.

38.   The nucleic acid of claim 37 wherein the nucleic acid comprises a nucleotide sequence selected from the group of nucleotide sequences set forth in Tables 1-134 or their complements.

39.   A substantially pure α-conotoxin protein precursor comprising an amino acid sequence selected from the group of amino acid sequences set forth in Tables 1-134.